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9 leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or
10 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to
11 nucleotide 62 of JS cp45, said genome or antigenome combined with one or more heterologous
12 gene(s) or genome segment(s) encoding one or more antigenic determinant(s) of HN and/or F
13 glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV genome or antigenome.

8/15/01

1 21. (Amended) The chimeric PIV of claim [1] 6, wherein the chimeric
2 genome or antigenome incorporates at least one and up to a full complement of attenuating
3 mutations present within HPIV3 JS cp45.

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1 22. (Amended) The chimeric PIV of claim [1] 6, wherein the chimeric
2 genome or antigenome incorporates at least one and up to a full complement of attenuating
3 mutations specifying an amino acid substitution in the L protein at a position corresponding to
4 Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of in JS cp45; in the N protein at a position corresponding to residues
5 Val₉₆ or Ser₃₈₉ of JS cp45, in the C protein at a position corresponding to Ile₉₆ of JS cp45, in
6 the F protein at a position corresponding to residues Ile₄₂₀ or Ala₄₅₀ of JS cp45, in the HN
7 protein at a position corresponding to residue Val₃₈₄ of JS cp45, a nucleotide substitution in a 3'
8 leader sequence of the chimeric virus at a position corresponding to nucleotide 23, 24, 28, or
9 45 of JS cp45, and/or a mutation in an N gene start sequence at a position corresponding to
10 nucleotide 62 of JS cp45.

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1 39. (Amended) An isolated polynucleotide comprising a chimeric
2 parainfluenza virus (PIV) genome or antigenome which includes a partial or complete human
3 parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome that incorporates at least
4 one and up to a full complement of attenuating mutations present within HPIV3 JS cp45
5 selected from mutations specifying an amino acid substitution in the L protein at a position
6 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS cp45; in the N protein at a position
7 corresponding to residues Val₉₆ or Ser₃₈₉ of JS cp45, in the C protein at a position
8 corresponding to Ile₉₆ of JS cp45, a nucleotide substitution in a 3' leader sequence of the
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS cp45,
11 said genome or antigenome combined with one or more heterologous gene(s) or genome

12 segment(s) encoding one or more antigenic determinant(s) of HN and/or F glycoproteins of
13 one or both of HPIV1 and HPIV2 to form a chimeric PIV genome or antigenome.

1 48. (Amended) A method for producing an infectious attenuated chimeric
2 parainfluenza virus (PIV) particle from one or more isolated polynucleotide molecules
3 encoding said PIV, comprising:

4 expressing in a cell or cell-free lysate an expression vector comprising an
5 isolated polynucleotide comprising a partial or complete human parainfluenza virus 3 JS
6 (HPIV3 JS) vector genome or antigenome that incorporates at least one and up to a full
complement of attenuating mutations present within HPIV3 JS cp45 selected from mutations
7 specifying an amino acid substitution in the L protein at a position corresponding to Tyr₉₄₂,
8 Leu₉₉₂, or Thr₁₅₅₈ of JS cp45; in the N protein at a position corresponding to residues Val₉₆ or
9 Ser₃₈₉ of JS cp45, in the C protein at a position corresponding to Ile₉₆ of JS cp45, a nucleotide
10 substitution in a 3' leader sequence of the chimeric virus at a position corresponding to
11 nucleotide 23, 24, 28, or 45 of JS cp45, and/or a mutation in an N gene start sequence at a
12 position corresponding to nucleotide 62 of JS cp45, said genome or antigenome combined with
13 one or more heterologous gene(s) or genome segment(s) encoding one or more antigenic
14 determinant(s) of HN and/or F glycoproteins of HPIV1 and/or HPIV2 to form a chimeric PIV
15 genome or antigenome, and PIV N, P, and L proteins.

1 50. (Amended) An expression vector comprising an operably linked
2 transcriptional promoter, a polynucleotide sequence which includes a partial or complete
3 human parainfluenza virus 3 JS (HPIV3 JS) vector genome or antigenome that incorporates at
4 least one and up to a full complement of attenuating mutations present within HPIV3 JS cp45
5 selected from mutations specifying an amino acid substitution in the L protein at a position
6 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS cp45; in the N protein at a position
7 corresponding to residues Val₉₆ or Ser₃₈₉ of JS cp45, in the C protein at a position
8 corresponding to Ile₉₆ of JS cp45, a nucleotide substitution in a 3' leader sequence of the
9 chimeric virus at a position corresponding to nucleotide 23, 24, 28, or 45 of JS cp45, and/or a
10 mutation in an N gene start sequence at a position corresponding to nucleotide 62 of JS cp45,
11 said genome or antigenome combined with one or more heterologous gene(s) or genome

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